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 JUN 12 2001
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<110> JENTICH, Thomas A.

<121> NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS

<130> 2825-1272

<140> 19-490,361

<141> 2000-11-27

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 1335

<212> DNA

<213> Homo sapiens

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<221> gene

<222> (1)..(2335)

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 Met Ala Glu Ala Pro Pro Arg Arg Leu Gly
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ctc ggt ccc ccg ccc ggg gac gcc ccc cgc ggc gag cta gtc ggc ctc 160
 Leu Gly Pro Pro Pro Gly Asp Ala Pro Arg Ala Glu Leu Val Ala Leu
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aag gcc gtg cag agc gaa cag gcc gag gcc gcc ggg gcc gcc tcc ccg 208
 Thr Ala Val Gln Ser Glu Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro
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cgc cgc ctc gcc ctc ctg gcc agc ccc ctg ccg ccg gcc gcc ccc ctc 256
 Arg Arg Leu Gly Leu Leu Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu
 45 50 55

cct ggg ccg gcc tcc gcc tcg gcc tcc gcc tgc gcc cag cgc tcc tcg 304
 Pro Gly Pro Gly Ser Gly Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser
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gcc gcc cac aag cgc tac cgc cgc ctg cag aac tgg gtc tac aac gtg 352
 Ala Ala His Lys Arg Tyr Arg Arg Leu Gln Asn Trp Val Tyr Asn Val
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ctc gag ccg ccc cgc gcc tgg gcc ttc gtc tac cag gtc ttc ata ttt 400

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Arg Glu Lys His Ile His Lys Arg Arg Met Pro Ala Ala Asn Leu Ile	340 345	
1164	cag ggt ggt tgg cgc ctg tac tcc acc gat atg agt ggt ggt tac ctg	1169
Gln Ala Ala Trp Arg Leu Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu	350 355 360	
1216	aca ggt acc tgg tac tac tat cac agt atc ctc cca tcc ttc ada gag	1226
Thr Ala Thr Trp Tyr Tyr Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu	365 370 375	
1264	ctg gcc ctc tgg ttt gag cac atg caa cgg gcc cgc aat ggg ggc cta	1269
Leu Ala Leu Leu Phe Glu His Val Gln Arg Ala Arg Asn Gly Gly Leu	380 385 390	
1312	cgg ccc ctg gag gtg cgg cgg cgg ccc gta ccc gac gga gca ccc tcc	1322
Arg Pro Leu Glu Val Arg Arg Ala Pro Val Pro Asp Gly Ala Pro Ser	395 400 405 410	
1360	cgt tac cgg ccc gtt gcc acc tgc cac cgg cgg ggc agc acc tcc ttc	1365
Arg Tyr Pro Pro Val Ala Thr Cys His Arg Pro Gly Ser Thr Ser Phe	415 420 425	
1408	tgc cct ggg gaa agc agc cgg atg ggc atc aaa gac cgc atc cgc atg	1418
Cys Pro Gly Glu Ser Ser Arg Met Gly Ile Lys Asp Arg Ile Arg Met	430 435 440	
1456	ggc agc tcc cag cgg cgg acc ggt cct tcc aag cag cag ctg gca cct	1466
Gly Ser Ser Gln Arg Arg Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro	445 450 455	
1504	cca aca atg ccc acc tcc cca agc agt gag cag gtg ggt gag gcc acc	1514
Pro Thr Met Pro Thr Ser Pro Ser Ser Glu Gln Val Gly Glu Ala Thr	460 465 470	
1552	agg ccc acc aag gtg caa aag agc tgg agc ttc aat gac cgc acc cgc	1562
Ser Pro Thr Lys Val Gln Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg	475 480 485 490	
1600	ttc cgg gca tct ctg aga ctc aaa ccc cgc acc tct gct gag gat gcc	1610
Phe Arg Ala Ser Leu Arg Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala	495 500 505	
1648	ccc tca gag gaa gta gca gag gag aag agc tac cag tgt gag ctc aag	1658
Pro Ser Glu Glu Val Ala Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr	510 515 520	
1696	gtg gac gac atc atg cct gct gtg aag aca gtc atc cgc tcc atc agg	1706
Val Asp Asp Ile Met Pro Ala Val Lys Thr Val Ile Arg Ser Ile Arg	525 530 535	
1744	att ctc aag ttc ctg gtg gcc aaa agg aaa ttc aag gag aca ctg cga	1754
Ile Leu Lys Phe Leu Val Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg	540 545 550	

1874
 Phe Tyr Asp Val Lys Asp Val Ile Ala Gln Tyr Ser Ala Gly His Leu
 601 605 610

1884
 Asp Met Leu Gly Arg Ile Lys Ser Leu Gln Thr Arg Val Asp Gln Ile
 606 611 616

1894
 Val Gly Arg Gly Pro Gly Asp Arg Lys Ala Arg Gln Lys Gly Asp Lys
 610 615 620

1906
 Gly Pro Ser Asp Ala Gln Val Val Asp Gln Ile Ser Met Met Gly Arg
 605 610 615

1984
 Val Val Lys Val Gln Lys Gln Val Gln Ser Ile Gln His Lys Leu Asp
 620 625 630

2032
 Leu Leu Leu Gly Phe Tyr Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala
 635 640 645 650

2080
 Ser Leu Gly Ala Val Gln Val Pro Leu Phe Asp Pro Asp Ile Thr Ser
 655 660 665

2128
 Asp Tyr His Ser Pro Val Asp His Glu Asp Ile Ser Val Ser Ala Gln
 670 675 680

2170
 Thr Leu Ser Ile Ser Arg Ser Val Ser Thr Asn Met Asp
 685 690 695

2230
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2290
 ctctcagggc tccggactcc tctcgtaact gaactcactc cctcacgggg agagagacca

2335
 cactgagtat tgagctgact gactggggcgt ggtacctgct gtggg

2210: 2
 2211: 695
 2212: PRT
 2213: Homo sapiens

2400: 2
 Met Ala Glu Ala Pro Pro Arg Arg Leu Gly Leu Gly Pro Pro Pro Gly
 1 5 10 15
 Asp Ala Pro Arg Ala Glu Leu Val Ala Leu Thr Ala Val Gln Ser Glu
 20 25 30
 Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro Arg Arg Leu Gly Leu Leu
 35 40 45
 Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu Pro Gly Pro Gly Ser Gly

Ser	Gly	Ser	Ala	Lys	Gly	Gln	Asn	Ser	Ser	Ala	Ala	His	Lys	Asn	Tyr	
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Arg	Arg	Leu	Gln	Asn	Trp	Val	Tyr	Asn	Val	Leu	Gln	Arg	Pro	Arg	Gly	
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Trp	Ala	Phe	Val	Tyr	His	Val	Phe	Ile	Phe	Leu	Leu	Val	Phe	Ser	Cys	
				107				115					110			
Leu	Val	Leu	Ser	Val	Leu	Ser	Thr	Ile	Gln	Gln	His	Gln	Gln	Leu	Ala	
				118				120				128				
Asn	Gln	Cys	Leu	Leu	Ile	Leu	Gln	Phe	Val	Met	Ile	Val	Val	Phe	Gly	
				130				135				140				
Leu	Gln	Tyr	Ile	Val	Arg	Val	Trp	Ser	Ala	Gly	Cys	Cys	Cys	Arg	Tyr	
				145				150				155			161	
Arg	Gly	Trp	Gln	Gly	Arg	Phe	Arg	Phe	Ala	Arg	Lys	Pro	Phe	Cys	Val	
				165					170					175		
Ile	Asp	Phe	Ile	Val	Phe	Val	Ala	Ser	Val	Ala	Val	Ile	Ala	Ala	Gly	
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Thr	Gln	Gly	Asn	Ile	Phe	Ala	Thr	Ser	Ala	Leu	Arg	Ser	Met	Arg	Phe	
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Leu	Gln	Ile	Leu	Arg	Met	Val	Arg	Met	Asp	Arg	Arg	Gly	Gly	Thr	Trp	
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Lys	Leu	Leu	Gly	Ser	Val	Val	Tyr	Ala	His	Ser	Lys	Gln	Leu	Ile	Thr	
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Ala	Trp	Tyr	Ile	Gly	Phe	Leu	Val	Leu	Ile	Phe	Ala	Ser	Phe	Leu	Val	
				245					250					255		
Tyr	Leu	Ala	Glu	Lys	Asp	Ala	Asn	Ser	Asp	Phe	Ser	Ser	Tyr	Ala	Asp	
				260				265					270			
Ser	Leu	Trp	Trp	Gly	Thr	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Tyr	Gly	Asp	
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Lys	Thr	Pro	His	Thr	Trp	Leu	Gly	Arg	Val	Leu	Ala	Ala	Gly	Phe	Ala	
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Leu	Leu	Gly	Ile	Ser	Phe	Ala	Leu	Pro	Ala	Gly	Ile	Leu	Gly	Ser		
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Gly	Phe	Ala	Leu	Lys	Val	Gln	Gln	Gln	His	Arg	Gln	Lys	His	Phe	Glu	
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Lys	Arg	Arg	Met	Pro	Ala	Ala	Asn	Leu	Ile	Gln	Ala	Ala	Trp	Arg	Leu	
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Tyr	Ser	Thr	Asp	Met	Ser	Arg	Ala	Tyr	Leu	Thr	Ala	Thr	Trp	Tyr	Tyr	
				355				360				365				
Tyr	Asp	Ser	Ile	Leu	Pro	Ser	Phe	Arg	Gln	Leu	Ala	Leu	Leu	Phe	Glu	
				370				375				380				
His	Val	Gln	Arg	Ala	Arg	Asn	Gly	Gly	Leu	Arg	Pro	Leu	Gln	Val	Arg	
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Arg	Ala	Pro	Val	Pro	Asp	Gly	Ala	Pro	Ser	Arg	Tyr	Pro	Pro	Val	Ala	
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Thr	Gly	Pro	Ser	Lys	Gln	Gln	Leu	Ala	Pro	Pro	Thr	Met	Pro	Thr	Ser	
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Pro	Ser	Ser	Glu	Gln	Val	Gly	Gln	Ala	Thr	Ser	Pro	Thr	Lys	Val	Gln	
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Lys	Ser	Trp	Ser	Phe	Asn	Asp	Arg	Thr	Arg	Phe	Arg	Ala	Ser	Leu	Arg	
				485					490					495		
Leu	Lys	Pro	Arg	Thr	Ser	Ala	Glu	Asp	Ala	Pro	Ser	Glu	Glu	Val	Ala	
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611 Ala Lys Ser Tyr Gln Lys Ala Leu Ile Val Asp Asp Ile Met Trp
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 613 Ala Val Lys Thr Val Ile Arg Ser Ile Arg Ile Leu Lys His Leu Val
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 615 Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg His Tyr Asp Val Lys Asp
 616
 617 Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Gly Arg Ile
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 619 Lys Ser Leu Gln Thr Arg Val Asp Gln Ile Val Gly Arg Gly Pro Gly
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 621 Asp Arg Lys Ala Arg Gln Lys Gly Asp Lys Gly Pro Ser Asp Ala Gln
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 623 Val Val Asp Glu Ile Ser Met Met Gly Arg Val Val Lys Val Gln Lys
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 625 Gln Val Gln Ser Ile Glu His Lys Leu Asp Leu Leu Gly Phe Tyr
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 627 Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala Ser Leu Gly Ala Val Gln
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 629 Val Pro Leu Phe Asp Pro Asp Ile Thr Ser Asp Tyr His Ser Pro Val
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*0210> Description of Artificial Sequence: PCR Primer

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*0210> 6

*0211> 21

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*0213> Artificial Sequence

*0220>

*0223> Description of Artificial Sequence: PCR Primer

*4001> 6

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21

*0210> 7

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*0213> Artificial Sequence

*0220>

*0223> Description of Artificial Sequence: PCR Primer

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*0210> 8

*0211> 20

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*0223> Description of Artificial Sequence: PCR Primer

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 <223> Description of Artificial Sequence: PCR Primer

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 aacacggggtt gacacacc 18

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 <430> 17
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11/11/11 11:11:11

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<223> Description of Artificial Sequence: PCR Primer

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gctggcttcaatctt

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<212> DNA

<213> Artificial Sequence

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<215> Description of Artificial Sequence: PCR Primer

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<211> 21

<212> DNA

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<223> Description of Artificial Sequence: PCR Primer

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<211> 676

<212> PRT

<213> Homo sapiens

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Trp Gly Arg Leu Pro Gly Ala Arg Arg Gly Ser Ala Gly Leu Ala Lys
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Lys Lys Ile Thr Ser Leu His Leu Ala His Gly Gly Ile Ala Gly Gly
 5
 Ala Leu Tyr Ala His Ile Ala His Gly Ala His Gly His Ala His His
 10
 Ala Ser Pro Ala Ala Pro Ala Ala Pro Pro Val Ala Ser Asp Leu Gly
 15
 Pro Arg Pro Pro Val Ser Leu Asp Pro Arg Val Ser Ile Tyr Ser Thr
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 Arg Arg Pro Val Leu Ala Arg Thr His Val Gln Gly Arg Val Tyr Asn
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 Phe Leu Glu Arg Pro Thr Gly Trp Lys Cys Phe Val Tyr His Phe Ala
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 Val Phe Leu Ile Val Leu Val Cys Leu Ile Phe Ser Val Leu Ser Thr
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 Ile Glu Gln Tyr Ala Ala Leu Ala Thr Gly Thr Leu Phe Trp Met Glu
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 Ile Val Leu Val Val Phe Phe Gly Thr Glu Tyr Val Val Arg Leu Trp
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 Ser Ala Gly Cys Arg Ser Lys Tyr Val Gly Leu Trp Gly Arg Leu Arg
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 Phe Ala Arg Lys Pro Ile Ser Ile Ile Asp Leu Ile Val Val Val Ala
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 Ser Met Val Val Leu Cys Val Gly Ser Lys Gly Gln Val Phe Ala Thr
 60
 Ser Ala Ile Arg Gly Ile Arg Phe Leu Gln Ile Leu Arg Met Leu His
 65
 Val Asp Arg Gln Gly Gly Thr Trp Arg Leu Leu Gly Ser Val Val Phe
 70
 Ile His Arg Gln Glu Leu Ile Thr Thr Leu Tyr Ile Gly Phe Leu Gly
 75
 Leu Ile Phe Ser Ser Tyr Phe Val Tyr Leu Ala Glu Lys Asp Ala Val
 80
 Asn Glu Ser Gly Arg Val Glu Phe Gly Ser Tyr Ala Asp Ala Leu Trp
 85
 Trp Gly Val Val Thr Val Thr Thr Ile Gly Tyr Gly Asp Lys Val Pro
 90
 Gln Thr Trp Val Gly Lys Thr Ile Ala Ser Cys Phe Ser Val Phe Ala
 95

340 Ser Ser His His Ala Leu Ile Ala Lys Ile Leu Lys Ser Lys Ile Ala
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11 Tyr Gly Ser Gly Gly Ser Val Arg Ile Ala Leu Ile Ile Ile Ile Ser
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Asn Thr Leu Pro Thr Tyr Ala Ala Leu Thr Val Ile Arg Arg Gly Pro
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Asp Glu Gly Ser
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 <211> PRT
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Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
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Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
 35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
 50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
 65 70 75 81

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
 85 90 95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
 100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
 115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
 130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
 145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
 165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
 180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
 195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
 210 215 220

Val Tyr Ala His Ser Lys Glu Ile Val Thr Ala Trp Tyr Ile Gly His
125 130 135 140 145 150 155 160 165 170 175 180 185 190

Leu Lys Leu Ile Leu Ala Ser His Leu Val Tyr Leu Ala Glu Lys Gly
195 200 205 210 215 220 225 230 235 240 245 250 255 260

Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
265 270 275 280 285 290 295 300 305 310 315 320 325 330

Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
335 340 345 350 355 360 365 370 375 380 385 390 395 400

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
405 410 415 420 425 430 435 440 445 450 455 460 465 470

Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
475 480 485 490 495 500 505 510 515 520 525 530 535 540

Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
545 550 555 560 565 570 575 580 585 590 595 600 605 610

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
615 620 625 630 635 640 645 650 655 660 665 670 675 680

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
685 690 695 700 705 710 715 720 725 730 735 740 745 750

Val Pro Met Tyr Arg Leu Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu
755 760 765 770 775 780 785 790 795 800 805 810 815 820

Arg Asn Leu Lys Ser Lys Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro
825 830 835 840 845 850 855 860 865 870 875 880 885 890

Pro Glu Pro Ser Pro Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe
895 900 905 910 915 920 925 930 935 940 945 950 955 960

Ser Ser Pro Arg Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala
965 970 975 980 985 990 995 1000 1005 1010 1015 1020 1025 1030

Gln Thr Val Arg Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser
1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100

Pro Ser Lys Val Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala
1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170

Arg Gln Ala Phe Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu
1175 1180 1185 1190 1195 1200 1205 1210 1215 1220 1225 1230 1235 1240

Glu Ala Ser Leu Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro
1245 1250 1255 1260 1265 1270 1275 1280 1285 1290 1295 1300 1305 1310

Cys Glu Phe Val Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile
1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380

Arg Ala Val Cys Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys
1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450

His Ser Leu Arg Pro	Tyr Arg Val Met Arg Val	Ile Glu Glu Thr Ser	647
Ala Gly His Leu Asp Met Leu Ser Arg	Ile Lys Ser Leu Glu Ser Arg	648	651
Val Asp Glu Ile Val Gly Arg Gly Pro	Ala Ile Thr Asp Lys Asp Arg	660	670
Thr Lys Gly Pro Ala Glu Ala Glu Leu Pro	Glu Asp Pro Ser Met Met	681	690
Gly Arg Leu Gly Lys Val Glu Lys Glu Val	Leu Ser Met Glu Lys Lys	695	700
Leu Asp Phe Leu Val Asn Ile Tyr Met	Gln Arg Met Gly Ile Pro Pro	610	620
Thr Glu Thr Glu Ala Tyr Phe Gly Ala	Lys Glu Pro Glu Pro Ala Pro	625	640
Pro Tyr His Ser Pro Glu Asp Ser Arg	Glu His Val Asp Arg His Gly	645	655
Cys Ile Val Lys Ile Val Arg Ser Ser	Ser Ser Thr Gly Gln Lys Asn	660	670
Phe Ser Ala Pro Pro Ala Ala Pro Pro	Val Gln Cys Pro Pro Ser Thr	675	685
Ser Trp Gln Pro Gln Ser His Pro Arg	Gln Gly His Gly Thr Ser Pro	690	700
Val Gly Asp His Gly Ser Leu Val Arg	Ile Pro Pro Pro Pro Ala His	705	720
Glu Arg Ser Leu Ser Ala Tyr Gly Gly	Gly Asn Arg Ala Ser Met Glu	725	735
Phe Leu Arg Gln Glu Asp Thr Pro Gly	Cys Arg Pro Pro Glu Gly Thr	740	750
Leu Arg Asp Ser Asp Thr Ser Ile Ser	Ile Pro Ser Val Asp His Glu	755	765
Glu Leu Glu Arg Ser Phe Ser Gly Phe	Ser Ile Ser Gln Ser Lys Glu	770	780
Asn Leu Asp Ala Leu Asn Ser Cys Tyr	Ala Ala Val Ala Pro Cys Ala	785	800
Lys Val Arg Pro Tyr Ile Ala Glu Gly	Glu Ser Asp Thr Asp Ser Asp	805	815
Leu Cys Thr Pro Cys Gly Pro Pro Pro	Arg Ser Ala Thr Gly Glu Gly	820	830

Met Gly Asp Val Gly Trp Ala Gly Phe Arg Lys
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<410> 38
Met Gly Leu Lys Ala Arg Arg Ala Ala Gly Ala Ala Gly Gly Gly Gly
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Asp Gly Gly Gly Gly Gly Gly Gly Ala Ala Asn Pro Ala Gly Gly Asp
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Ala Ala Ala Ala Gly Asp Glu Glu Arg Lys Val Gly Leu Ala Pro Gly
35 40 45

Asp Val Glu Gln Val Thr Leu Ala Leu Gly Ala Gly Ala Asp Lys Asp
50 55 60

Gly Thr Leu Leu Leu Glu Gly Gly Gly Arg Asp Glu Gly Gln Arg Arg
65 70 75 80

Thr Pro Gln Gly Ile Gly Leu Leu Ala Lys Thr Pro Leu Ser Arg Pro
85 90 95

Val Lys Arg Asn Asn Ala Lys Tyr Arg Arg Ile Gln Thr Leu Ile Tyr
100 105 110

Asp Ala Leu Glu Arg Pro Arg Gly Trp Ala Leu Leu Tyr His Ala Leu
115 120 125

Val Phe Leu Ile Val Leu Gly Cys Leu Ile Leu Ala Val Leu Thr Thr
130 135 140

Phe Lys Glu Tyr Glu Thr Val Ser Gly Asp Trp Leu Leu Leu Leu Glu
145 150 155 160

Thr Phe Ala Ile Phe Ile Phe Gly Ala Glu Phe Ala Leu Arg Ile Trp
165 170 175

Ala Ala Gly Cys Cys Cys Arg Tyr Lys Gly Trp Arg Gly Arg Leu Lys
180 185 190

Phe Ala Arg Lys Pro Leu Cys Met Leu Asp Ile Phe Val Leu Ile Ala
195 200 205

Ser Val Pro Val Val Ala Val Gly Asn Gln Gly Asn Val Leu Ala Thr
210 215 220

Ser Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met Leu Arg Met
225 230 235 240

Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Ala Ile Cys Ala

His Ser Lys Ala Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Thr Leu
 275 280 285
 Ile Leu Ser Ser Phe Leu Val Tyr Leu Val Ala Lys Asp Val Pro Glu
 290 295 300 305
 Val Asp Ala Gln Gly Glu Glu Met Lys Glu Glu Phe Glu Thr Tyr Ala
 310 315 320 325 330
 Asp Ala Leu Trp Trp Gly Leu Ile Thr Leu Ala Thr Ile Gly Tyr Gly
 335 340 345 350 355
 Asp Lys Thr Pro Lys Thr Trp Glu Gly Arg Leu Ile Ala Ala Thr Phe
 360 365 370 375 380
 Ser Leu Ile Gly Val Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly
 385 390 395 400 405
 Ser Gly Leu Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe
 410 415 420 425 430
 Glu Lys Arg Arg Lys Pro Ala Ala Glu Leu Ile Gln Ala Ala Trp Arg
 435 440 445 450 455
 Tyr Tyr Ala Thr Asn Pro Asn Arg Ile Asp Leu Val Ala Thr Trp Arg
 460 465 470 475 480 485
 Phe Tyr Glu Ser Val Val Ser Phe Pro Phe Phe Arg Lys Glu Gln Leu
 490 495 500 505 510 515
 Glu Ala Ala Ser Ser Gln Lys Leu Gly Leu Leu Asp Arg Val Arg Leu
 520 525 530 535 540 545
 Ser Asn Pro Arg Gly Ser Asn Thr Lys Gly Lys Leu Phe Thr Pro Leu
 550 555 560 565 570 575
 Asn Val Asp Ala Ile Glu Glu Ser Pro Ser Lys Glu Pro Lys Pro Val
 580 585 590 595 600 605
 Gly Leu Asn Asn Lys Glu Arg Phe Arg Thr Ala Phe Arg Met Lys Ala
 610 615 620 625 630 635
 Tyr Ala Phe Trp Gln Ser Ser Glu Asp Ala Gly Thr Gly Asp Pro Met
 640 645 650 655 660 665
 Ala Glu Asp Arg Gly Tyr Gly Asn Asp Phe Pro Ile Glu Asp Met Ile
 670 675 680 685 690 695
 Pro Thr Leu Lys Ala Ala Ile Arg Ala Val Arg Ile Leu Gln Phe Arg
 700 705 710 715 720 725
 Leu Tyr Lys Lys Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys
 730 735 740 745 750 755
 Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Ser Arg

14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
 Ile Lys Tyr Leu Val Thr Arg Ile Asp Met Ile Phe Thr Leu Gly Phe
 570 571 572
 Pro Ser Thr Pro Lys His Lys Lys Ser Gln Lys Gly Ser Ala Phe Thr
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 Phe Pro Ser Gln Gln Ser Pro Arg Asn Gln Pro Tyr Val Ala Arg Pro
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 Ser Thr Ser Gln Ile Gln Asp Gln Ser Met Met Gly Lys Phe Val Lys
 610 615 620
 Val Gln Arg Gln Val Gln Asp Met Gly Lys Lys Leu Asp Phe Leu Val
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 Asp Met His Met Gln His Met Gln Arg Leu Gln Val Gln Val Thr Gln
 645 650 655
 Tyr Tyr Pro Thr Lys Gly Thr Ser Ser Pro Ala Gln Ala Gln Lys Lys
 660 665 670
 Glu Asp Asn Arg Tyr Ser Asp Leu Lys Thr Ile Ile Cys Asn Tyr Ser
 675 680 685
 Glu Thr Gly Pro Pro Gln Pro Pro Tyr Ser Phe His Gln Val Thr Ile
 690 695 700
 Asp Lys Val Ser Pro Tyr Gly Phe Phe Ala His Asp Pro Val Asn Leu
 705 710 715 720
 Pro Arg Gly Gly Pro Ser Ser Gly Lys Val Gln Ala Thr Pro Pro Ser
 725 730 735
 Ser Ala Thr Thr Tyr Val Gln Arg Pro Thr Val Leu Pro Ile Leu Thr
 740 745 750
 Leu Leu Asp Ser Arg Val Ser Cys His Ser Gln Ala Asp Leu Gln Gly
 755 760 765
 Pro Tyr Ser Asp Arg Ile Ser Pro Arg Gln Arg Arg Ser Ile Thr Arg
 770 775 780
 Asp Ser Asp Thr Pro Leu Ser Leu Met Ser Val Asn His Glu Glu Leu
 785 790 795 800
 Glu Arg Ser Pro Ser Gly Phe Ser Ile Ser Gln Asp Arg Asp Asp Tyr
 805 810 815
 Val Phe Gly Pro Asn Gly Gly Ser Ser Trp Met Arg Glu Lys Arg Tyr
 820 825 830
 Leu Ala Gln Gly Glu Thr Asp Thr Asp Thr Asp Pro Phe Thr Pro Ser
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 Gly Ser Met Pro Leu Ser Ser Thr Gly Asp Gly Ile Ser Asp Ser Val

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1.00.

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 36
aagggtggat cagtcattg g 21

<210> 37
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 37
aaggggcag gctgttgctg g 21

<210> 38
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 38
atgggcac ctccccctg g 21

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 39
cccttgcaa ttagggcct gac 23

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<11> Artificial Sequence

<111>

<112> Description of Artificial Sequence: PCR Primer

<411> 41

ccaaataatg aacatcatgt agc

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<111> 41

<111> 24

<112> DNA

<113> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

<400> 41

cagaagagtc aagatgggca ggac

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